AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting at page 10, line 9 with the following:

Figure 9 shows the localization and the distinct sequences of alleles, ~~partial sequence of~~ *LAPTM4B* alleles of this invention *LAPTM4B**1 and *LAPTM4B**2. Figure 9-A indicates the localization of *LAPTM4B* alleles at 5'UTR of the first exon. Figure 9-B shows the distinct sequences of *LAPTM4B**1 and *LAPTM4B**2 alleles, wherein the underlined sequences are, respectively, a 19-bp sequence contained specifically in *LAPTM4B**1, and the tandem repeatedly arranged double 19-bp sequence contained specifically in *LAPTM4B**2.

Please replace the paragraph starting at page 10, line 12 with the following:

Figure 11 ~~is an immunohistochemical diagram of various cancer tissues derived from~~ shows the expression of LAPTM4B-35 protein in some epithelium derived cancrs by immunohistochemistry, wherein Figures 11-A, 11-C, 11-E, and 11-G show the negative staining of normal tissues, *i.e.* esophageal mucous, mammary gland tissue, lung tissue, and gastric mucous, respectively; and Figures 11-B, 11-D, 11-F, and 11-H show the staining of cancer tissues, *i.e.* negatively stained esophageal carcinoma, positively stained breast cancer, lung cancer, and gastric cancer, respectively.

Please replace the paragraph starting at page 10, line 16 with the following:

Figure 13 ~~13-A, B, C, D, and E are the Western blot analysis diagrams showing respectively that the expressions of cyclin D1, cyclin E, c-Myc, c-Fos, and c-Jun of cDNA-transfected cells of this invention are upregulated~~ shows the up-regulation of some cell cycle regulators and proto-oncogenes by transfection of *LAPTM4B*-cDNA (AE) Figures 13-A and 13-B show the up-regulation of cyclin D1 and cyclin E in *LAPTM4B*-overexpressed HLE-AE cells, respectively; Figures 13-C, 13-D, and 13-E show the up-regulation of c-Myc, c_jun, and c-Fos in *LAPTM4B*-overexpressed HLE-AE cells, respectively.

Please replace the paragraph starting at page 10, line 29 with the following:

Figure 17 is a plot showing the transcriptive activity of various fragments of *LAPTM4B* promoter of this invention shows the marked promoter sequence and the identification of transcriptional activity. Figure 17-A shows the *LAPTM4B* promoter sequence, wherein the potential targeting sequences of some transcription factors are underlined. Figure 17-B shows at the left part the promoter-reporter plasmids. The numbers indicate the position of the start point of the fragments related to the transcription start site; the right part is a plot showing the transcriptive activity of various fragments of *LAPTM4B* promoter in the present invention in BEL-7402 and HLE cells. Values of luciferase activity was represented as mean ± SD (N=6).

Please replace the paragraph starting at page 13, line 5 with the following:

By using the same procedures for the promoter sequence cloning, two primers, F1: 5' GCGCTCGAGGCTCCAGGTG GAAGAGTGTGC 3' (SEQ ID No: 11) (inducing XhoI enzyme cutting site at 5' terminal sequence as indicated by underlining), and R1: 5' GCGAAGCTT GGACTTGGCCATGTGACCCG 3' (SEQ ID No: 15) (inducing XhoI enzyme cutting site at 5' terminal sequence as indicated by underlining), were designed and synthesized based on *LAPTM4B* gene sequence SEQ ID No. 3. The promoter sequence and its anterior sequence in the first exon of *LAPTM4B* were then cloned from human genomic DNA by PCR. The pGL3-PF1 vectors constructed from various human genomic DNA were sequenced to screen the *LAPTM4B* alleles. The original *LAPTM4B* sequence was designated as *LAPTM4B**1. The other one was designated as *LAPTM4B**2, i.e., SEQ ID No. 6 in the sequence listings. FIG. 9(A) shows the schematic diagrams of the *LAPTM4B* promoter and its first exon. The rectangle frame indicates the first exon, the black color area represents the encoding area, the white color is the non-coded area, and the gray area shows a 19 bp DNA sequence. The horizontal line representing promoter part and F1, F2, R1, and R2 are where the four primers are located. "A" in the start codon ATG is defined as +1 in the sequence. FIG. 9 (B) shows the partial sequences of the *LAPTM4B* alleles and their sequencing graphic spectra. The underlined part is a 19 bp DNA sequence. The results reveal that *LAPTM4B**1 contains one copied 19 bp DNA sequence and *LAPTM4B**2 has two

copied 19 bp DNA sequences, which are linked in the non-coded area (nt -33--15) of the first exon of *LAPTM4B**1.

Please replace the paragraph starting at page 13, line 31 with the following:

E2 (5' GCCGACTAGGGGACTGGCGGA 3') (SEQ ID No: 9) and R2 (5' CGAGAGCTCCGAGCTTCTGCC 3') (SEQ ID No:10) primers were designed and synthesized. A partial sequence of the first exon of *LAPTM4B* was amplified by PCR using templates of genomic DNA from normal people, hepatocellular carcinoma, and esophagus carcinoma tissues. PCR conditions were as follows: 96°C. pre-denature for 5 min; 94°C. for 30 s, 68°C. for 30 s, 72°C. for 1 min, 35 cycles; 72°C. for 5 min; then the PCR products were conducted to 2% Agarose gel electrophoresis analysis. FIG. 10 shows *LAPTM4* gene *1/*1, *1/*2, and *2/*2 three types in human population.

Please replace the paragraph starting at page 14, line 17 with the following:

The sequences of these primers are as follows:

F1: 5'GCGCTCGAG GCTCCAGGTGGA AGAGTGTGC 3 (nt-1341--1321) (SEQ ID No: 11)

F2: 5'GCGCTCGAG TAAAAACGCTGTGCCAGGCGT 3' (nt-881--861) (SEQ ID No: 12)

F3: 5'CGGCTCGAG TACCGGAAGCACAGCGAGGAT 3' (nt-558--538) (SEQ ID No: 13)

F4: 5'GCGCTCGAG AGTAGAAGGGAAGAAAATCGC 3' (nt-38--18) (SEQ ID No: 14)

R1: 5'GCGAAGCTT GGACTTGGCCATGTGACCCG 3' (nt 172-191) (SEQ ID No: 15)

Please replace the paragraph starting at page 20, line 20 with the following:

LAPTM4B genotypes in genomic DNA from blood of normal individuals and patients with hepatocellular carcinoma were detected by PCR. Two primers were designed and synthesized according to the flanking sequence of 19 bp DNA sequence in LAPTM4B gene sequence 3:

F2: 5' GCCGACTAGGGGACTGGCGGA 3' (SEQ ID No: 9)

R1: 5' CGAGAGCTCCGAGCTTCTGCC 3' (SEQ ID No: 10)